

FIGURE 1A

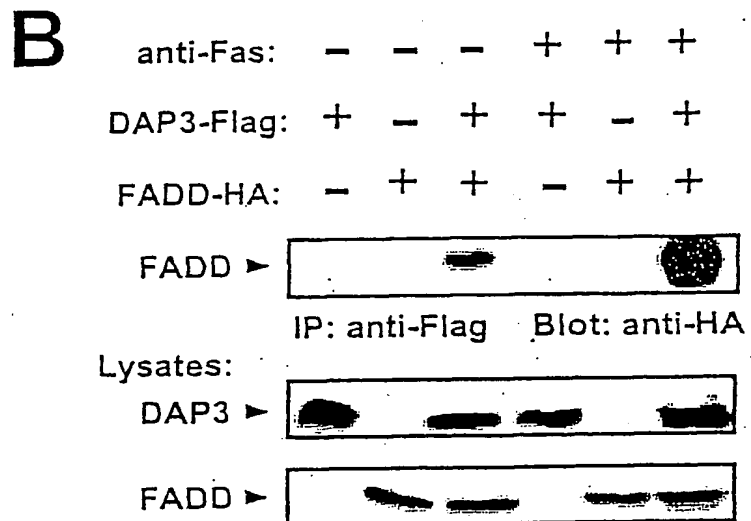


FIGURE 1B

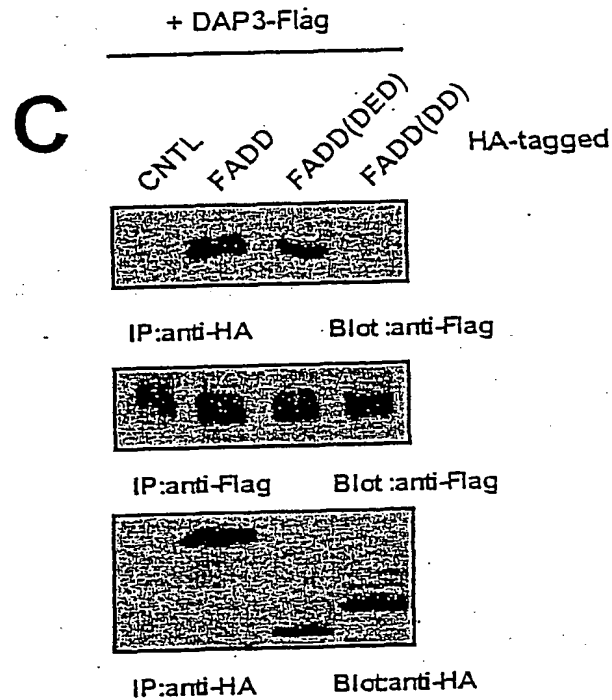


FIGURE 1C

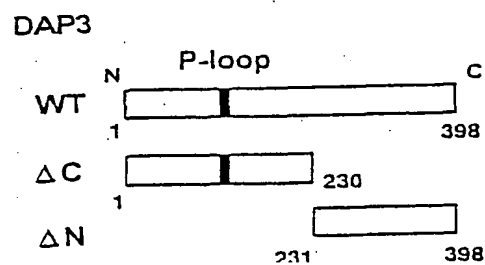
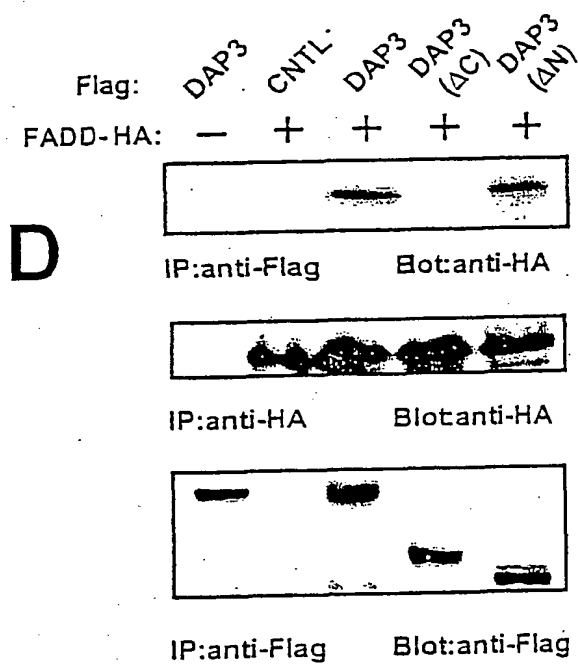


FIGURE 1D

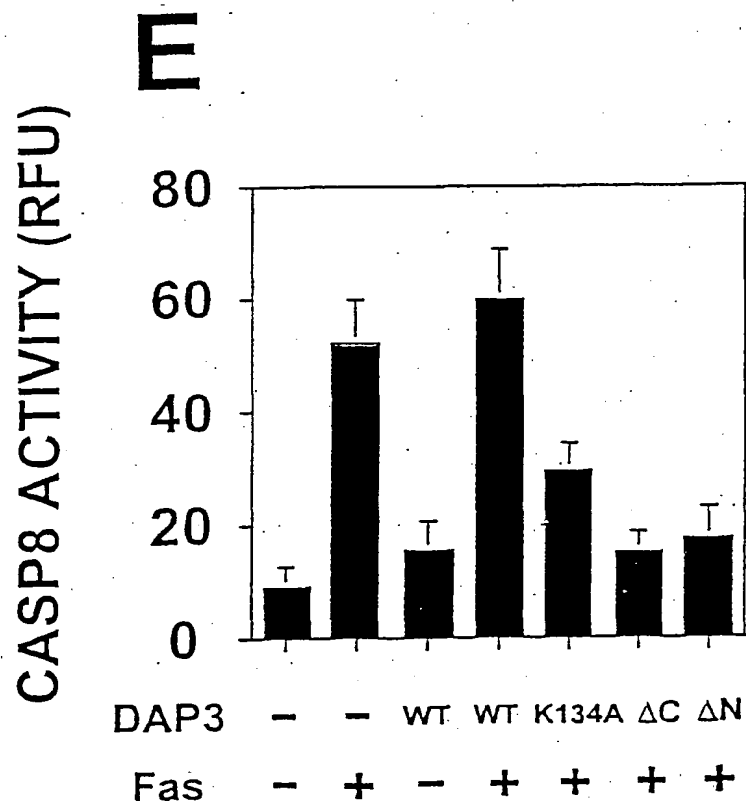


FIGURE 1E

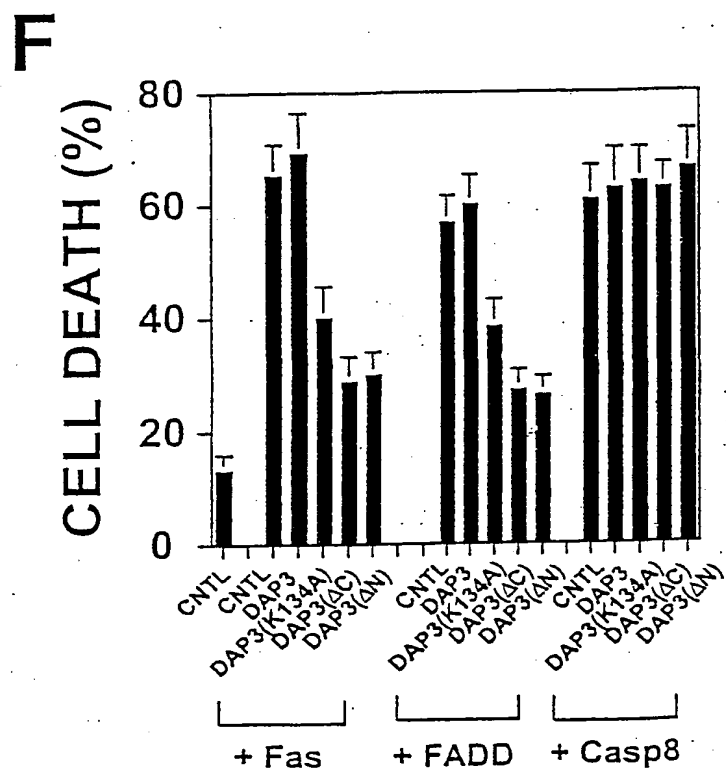


FIGURE 1F

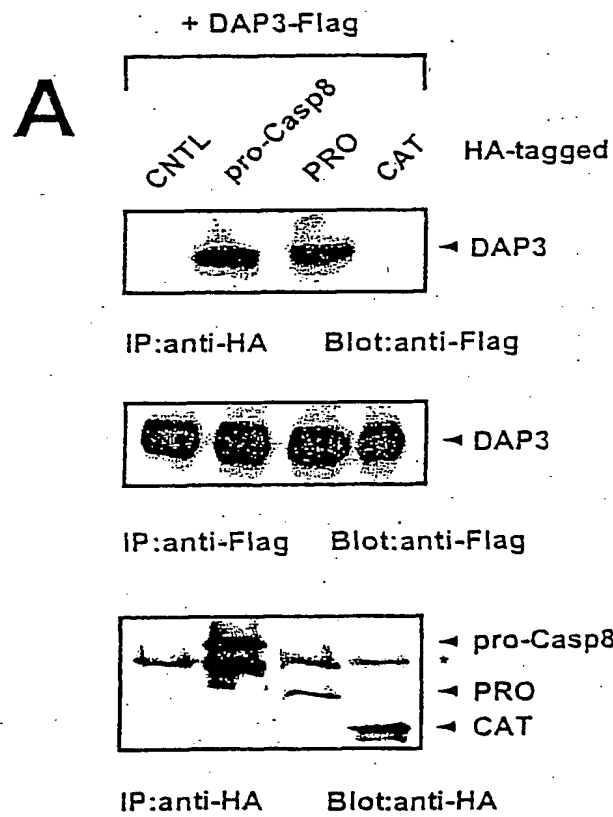


FIGURE 2A

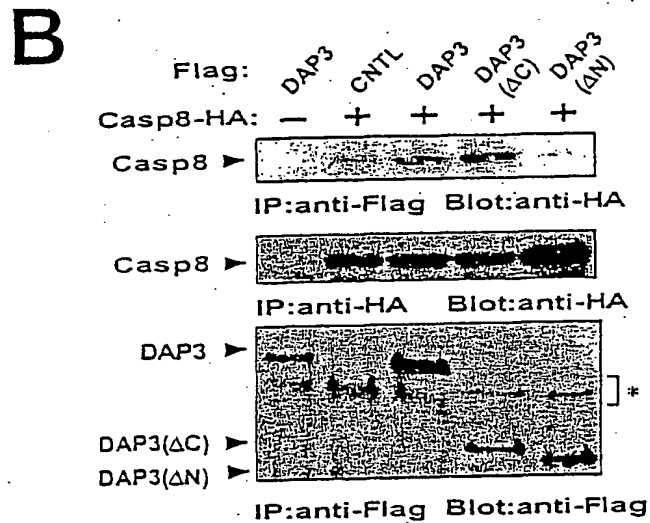


FIGURE 2B

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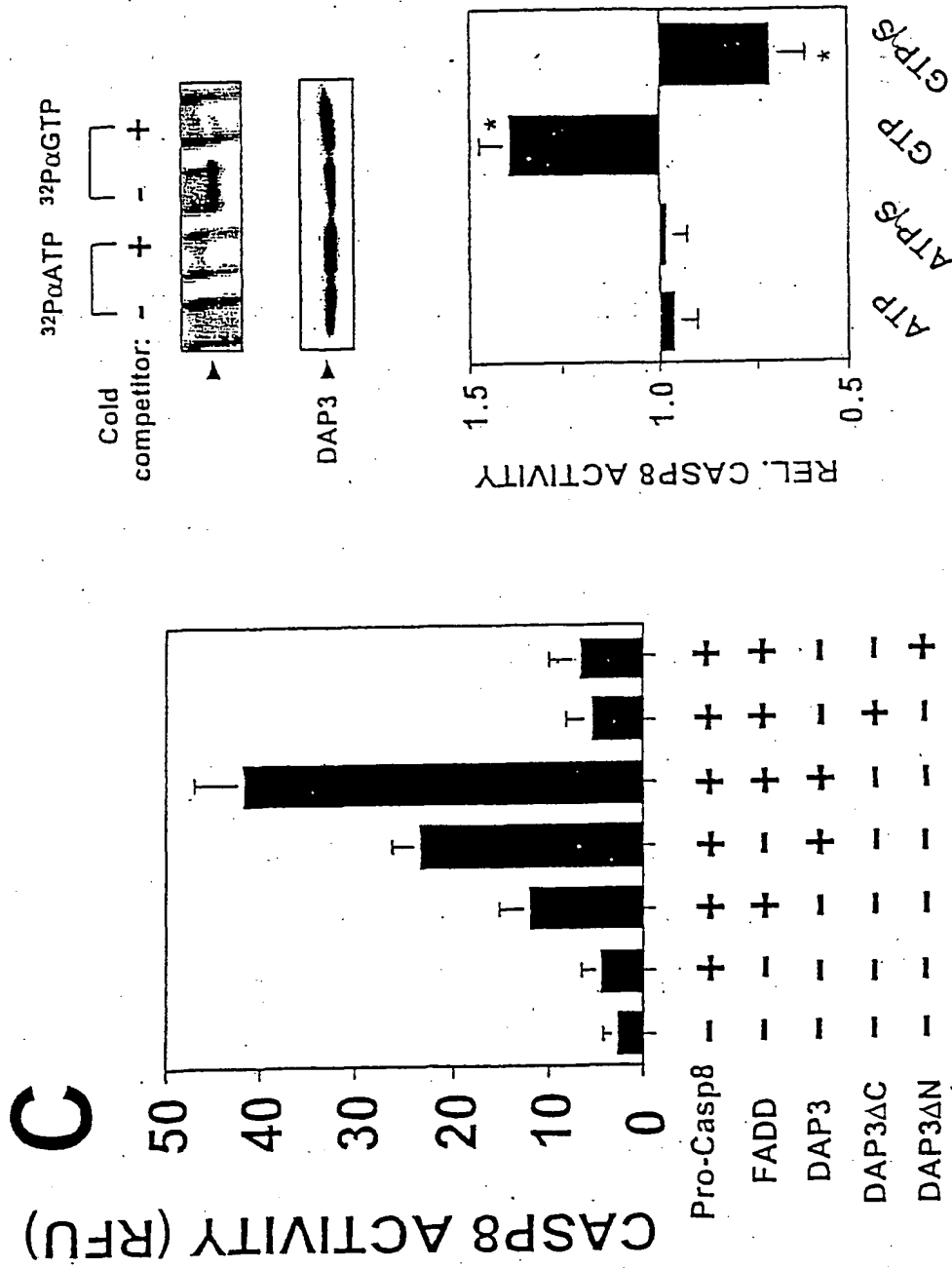


FIGURE 2C

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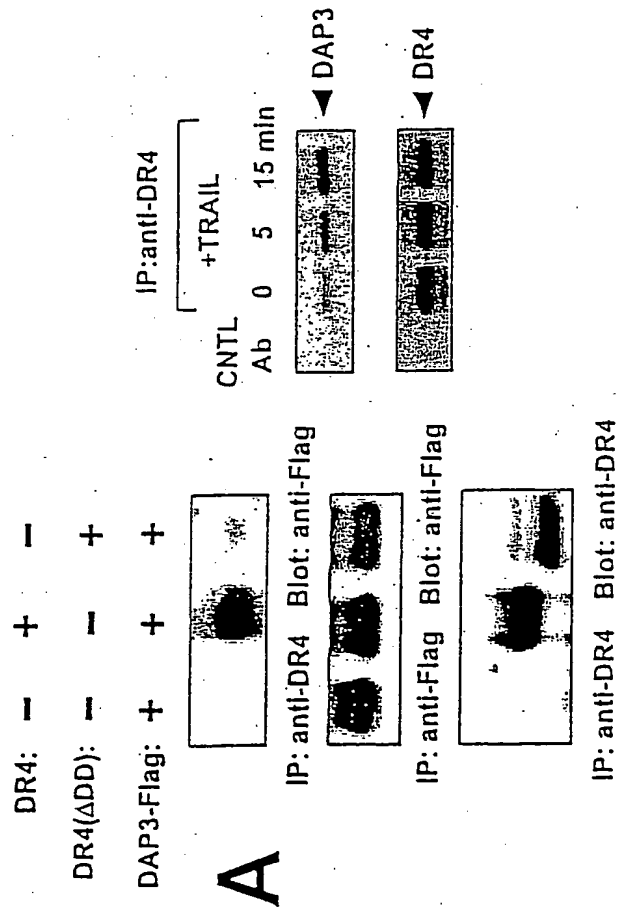


FIGURE 3A

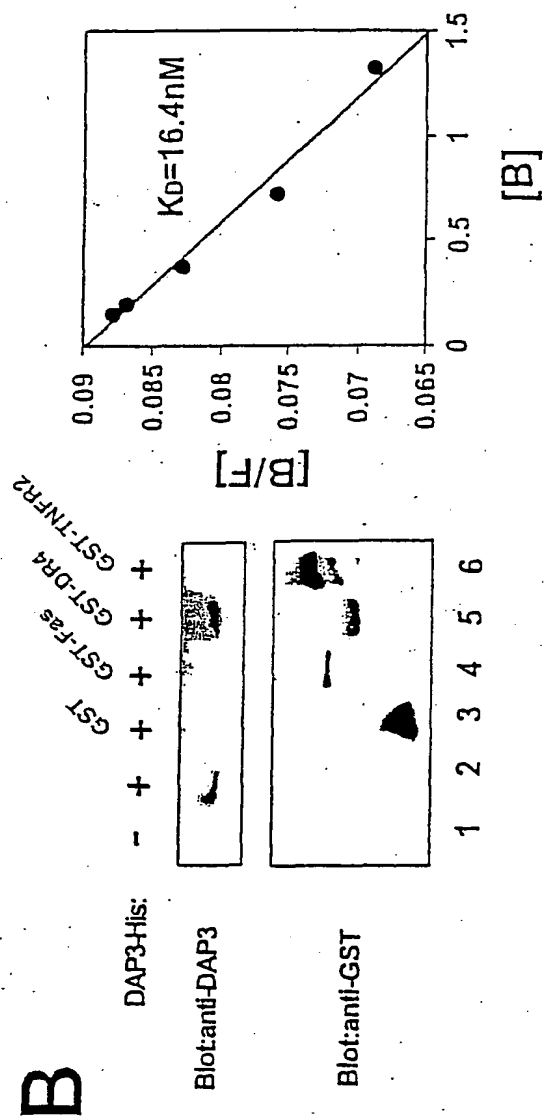


FIGURE 3B

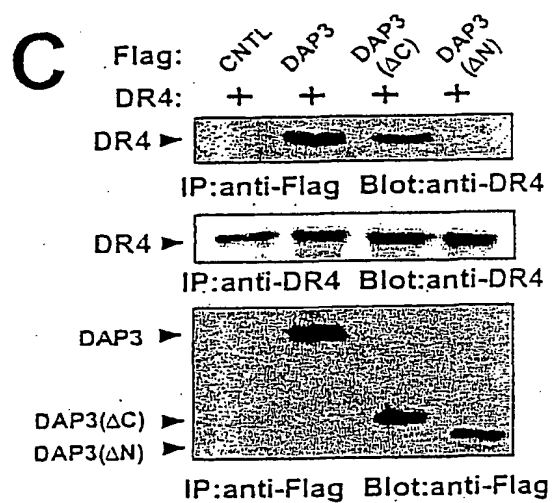


FIGURE 3C

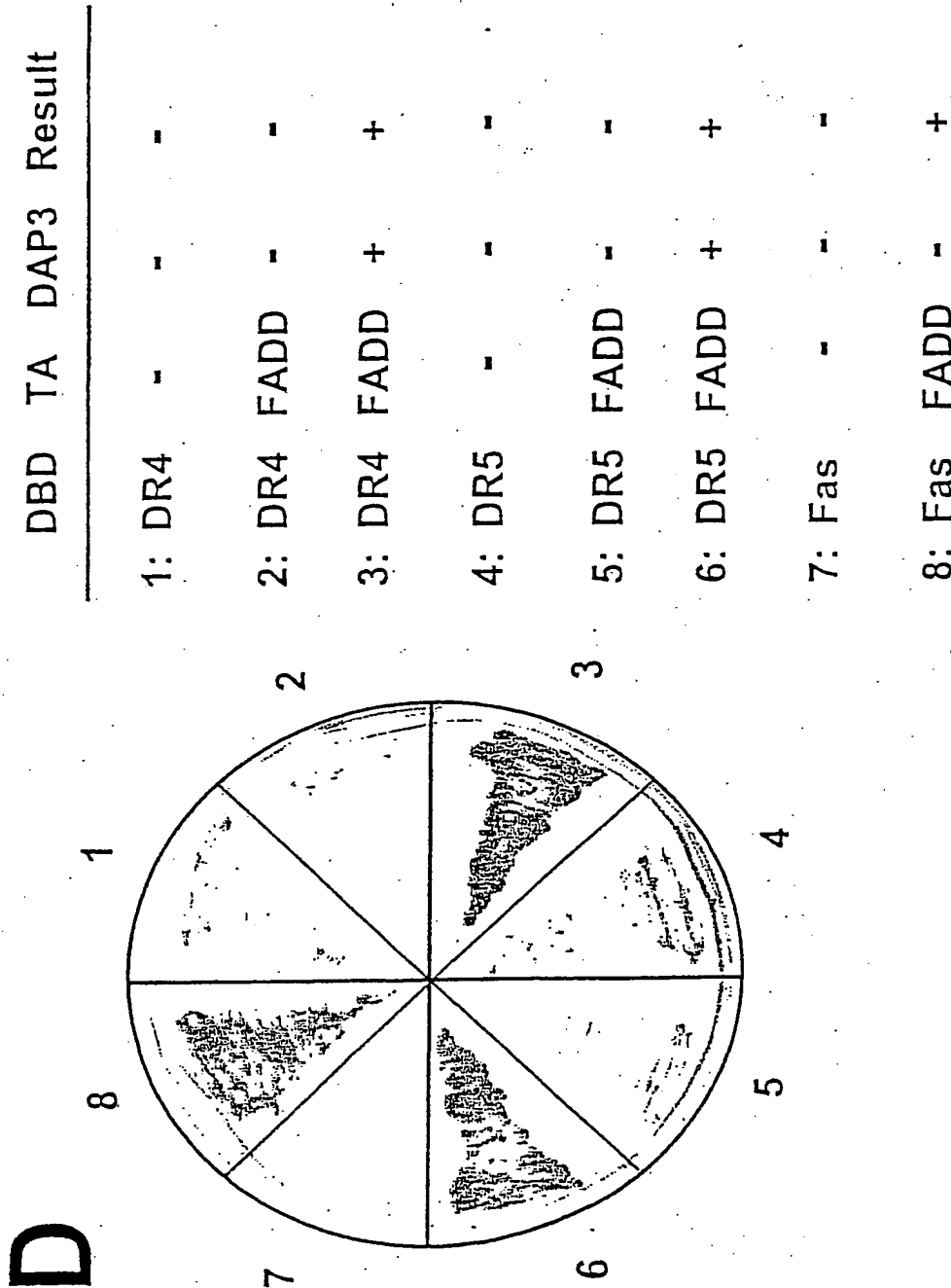


FIGURE 3D

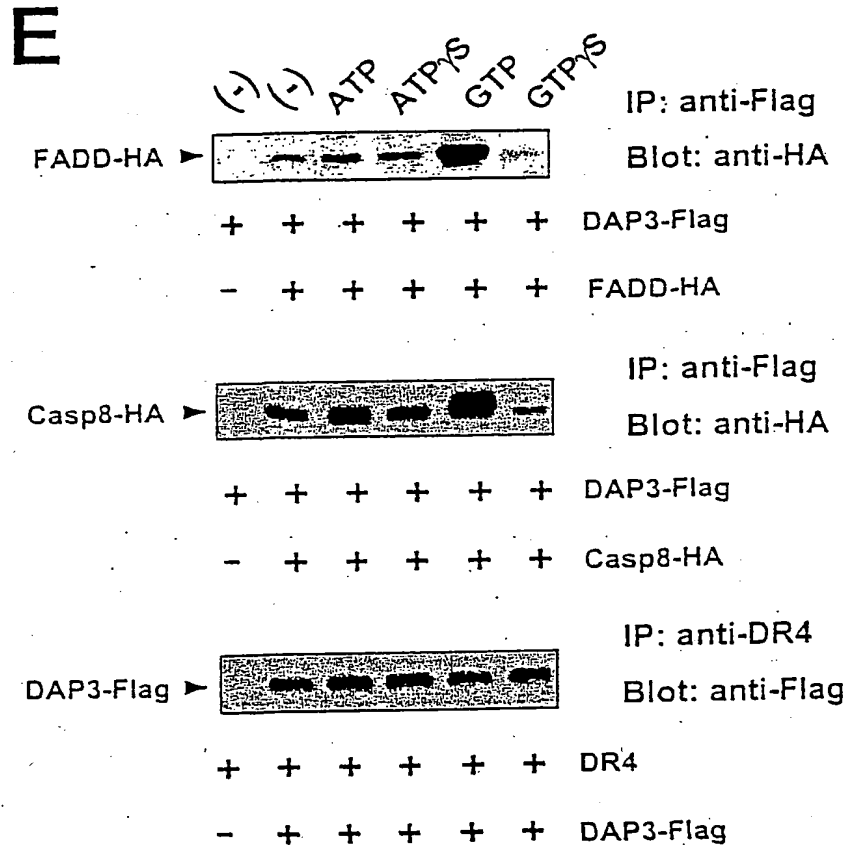


FIGURE 3E

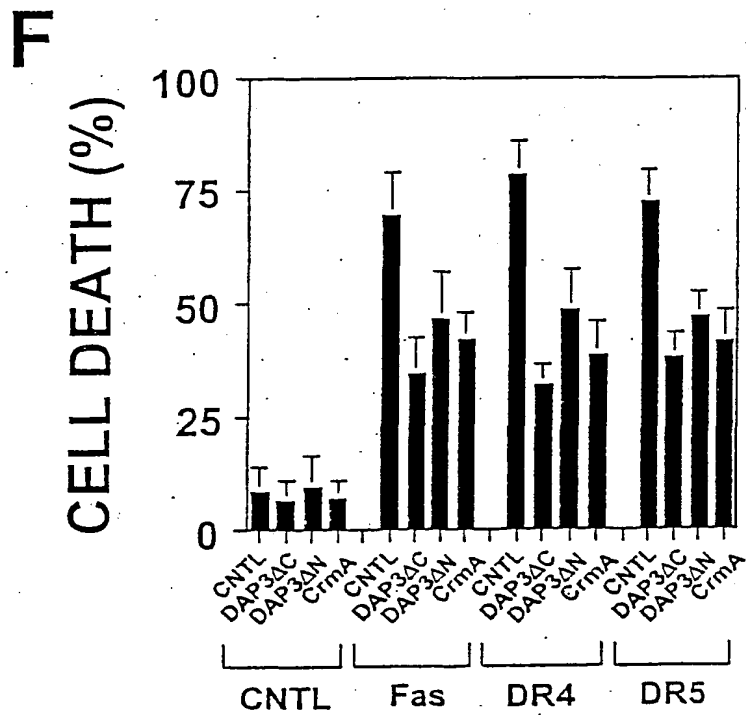


FIGURE 3F

G

DAP3
agtcctcga ctcacgtgca aggatgatgc tgaaaggaata

ant sense 1

ant sense 2

ant sense 3

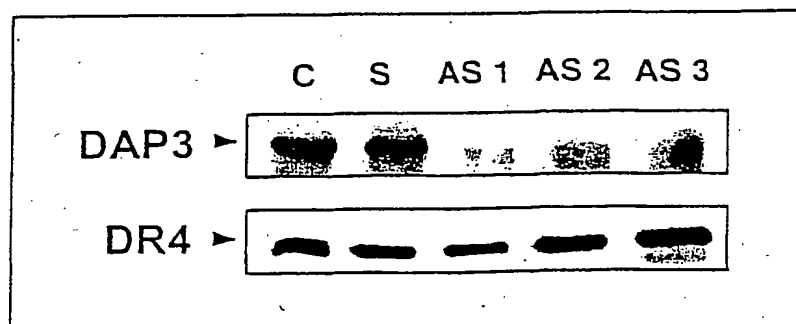
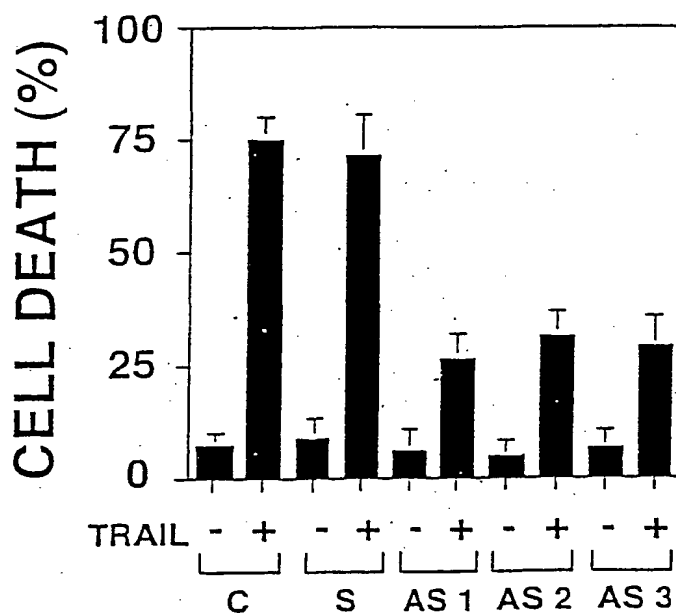


FIGURE 3G

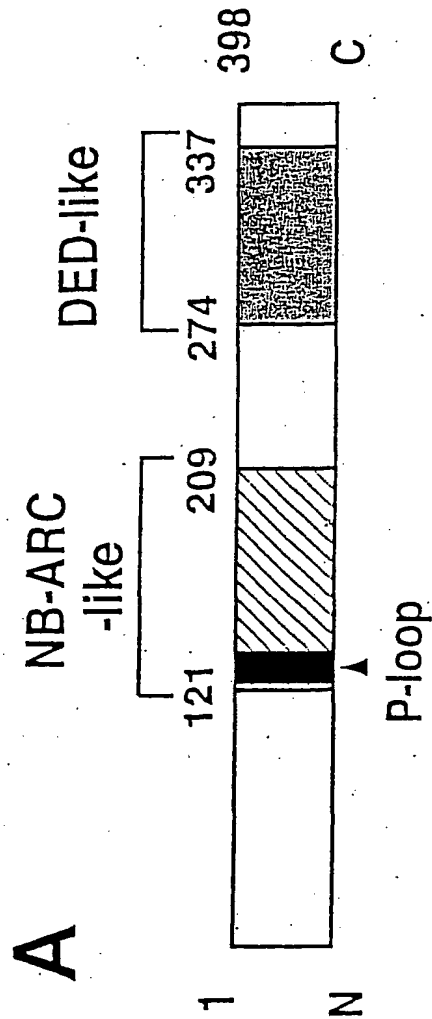
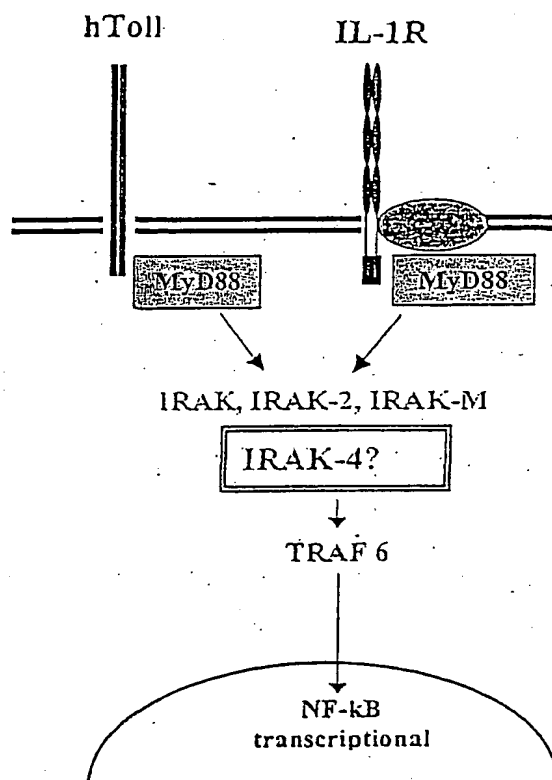


FIGURE 4A

1115	T S F A Y P A I R Y L L M G E K G L G K L E R S L C H V D N A	F C A K Q Q D W L	D A P 3
1142	K G - P G W V F L H G M A G C G K S V I A S O A	F F P G G V H W W L S V G K Q	A p a f 1 N
1146	E M C D L P S F L F L L H G A G S G K S V I A S O A	L I G I N Y D S V W L K D S G T	C E D 4
152	- - - - -	- - - - -	- - - - -
191	D K S G L L M K L Q D C T R L D Q D L S F S Q R L P L N E E A K D R L	H P D A H W V K N G R D L R Q S S Y	D A P 3
196	A P K S T F D L F T D L L M L K S E D L - L N F P S M E H V A L S V V L R M L G N A L	L R L R L R H P R	A p a f 1 N
174	N E K Q R F D Q P L E A S T - W - L K N F M - - - - -	L R Q S S Y	C E D 4
238	S L L L D D V W P S - - - - -	K Y V V W N K R	D A P 3
245	L F M F D D V V Q E E T I R W A - O L L R L R G - - - - -	M G P K Y V V E	A p a f 1 N
		A S Q T C E F V -	C E D 4

268	MD	WG	R	T	GL	LL	K	R	E	D	KS	P	EL	EL	EL	AL	W	H	N	L	F	L	S	DAP3 DED
1	MD	F	SR	N	LV	Q	I	SV	EL	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp8 DED1
98	H	L	L	I	R	V	M	L	Q	I	SV	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp8 DED2
17	K	V	S	F	R	E	K	L	I	I	SV	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp10 DED1
121	MD	FF	FR	LL	LV	EL	EL	EL	EL	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp10 DED2
1	MD	PP	LV	LL	LV	EL	EL	EL	EL	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	FADD DED
312	MD	T	GS	LF	K	P	R	K	A	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	DAP3 DED
50	EL	RR	M	LF	EE	GN	LL	D	EL	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp8 DED1
148	K	R	V	I	LF	EE	GN	LL	D	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp8 DED2
67	K	Q	G	K	LF	EE	GN	LL	D	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp10 DED1
167	E	Q	N	D	LF	EE	GN	LL	D	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	Casp10 DED2
51	E	Q	N	D	LF	EE	GN	LL	D	EL	EL	EL	EL	EL	EL	AL	W	H	N	L	F	L	S	FADD DED

FIGURE 4B, C

**FIGURE 5**

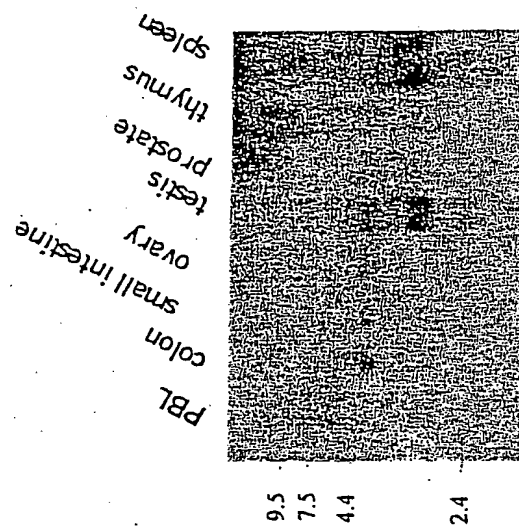


FIGURE 6

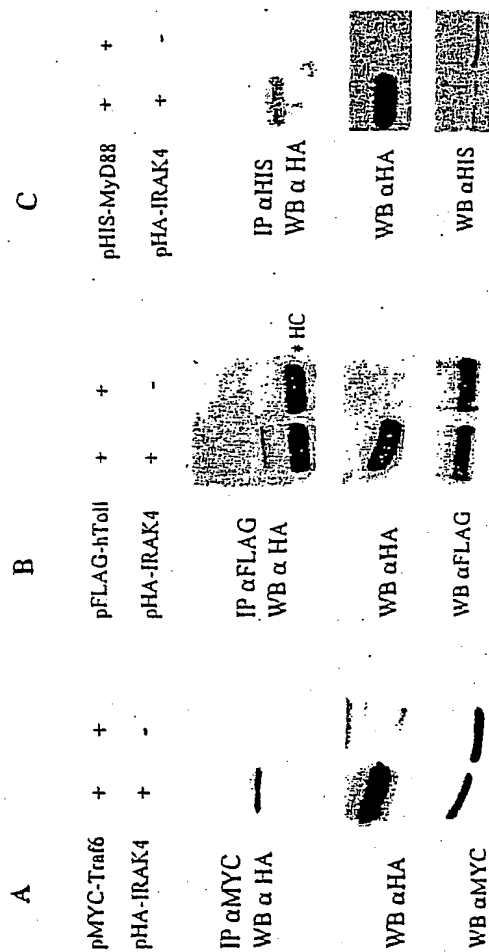


FIGURE 7

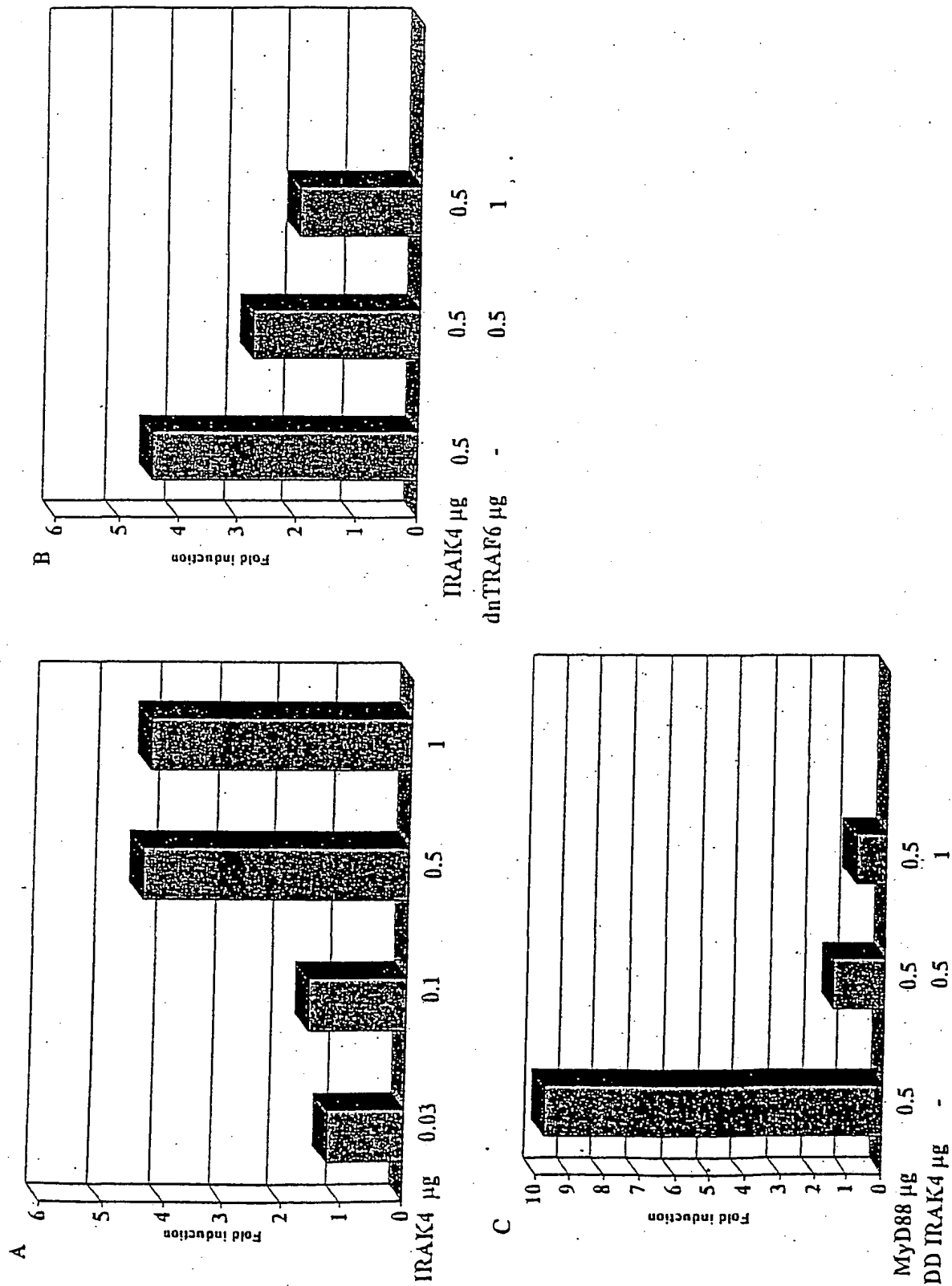


FIGURE 8

[illegible]

AAGG-----FA--A-SGGSEETERE--GQCDESNE-
HIIIG-----LUNG-EETATE-QG-CDESNE-
HIIIG-----LUNG-EETATE-QG-CDESNE-
PFGSPQANTPCP-ISA-SNO-MOPQEGCSAS-H-PISGVLEETE-GMSDAME-
-----VOSGDILSMCEMONDRPGF---

GOGL	PLA	HD	PH	PLA		PSP
GOGL	PLT	HD	PH	PLT		ACP
GOGL	PLT	HD	PH	PLT		ACP
GOGL	PLT	HD	PH	PLT		SP
BLASE	HD					VD

FIGURE 9

a tgaacaaacc cataacacca tcaacatatg tgcgctgcct caatgttggga ctaattagga agctgtcaga
ttttattgat cctcaagaag gatggaagaa gttagctgta gctattaaaa aaccatctgg
tgatgataga tacaatcagt ttcacataag gagatttgaa gcattacttc aaactggaaa
aagtcccact tctgaattac tgtttgactg gggcaccaca aattgcacag ttggtgatct
tgttgatcct ttgatccaaa atgaattttt tgctcctgcg agtcttttgc tcccagatgc
tgttcccaaa actgctaata cactaccttc taaagaagct ataacagttc agcaaaaaaca
gatgcctttc tgtgacaaag acaggacatt gatgacacct gtgcagaatc ttgaacaaag
ctatatgccca cctgactcct caagtccaga aaataaaagt ttagaagtta gtgatacacg
ttttcacagt ttttcatttt atgaattgaa gaatgtcaca aataactttg atgaacgacc
catttctgtt ggtggttaata aaatgggaga gggaggattt ggagttgtat ataaaggcta
cgtaaaataac acaactgtgg cagtgaagaa gcttgcagca atgggttgaca ttactactga
agaactgaaa cagcagtttg atcaagaaat aaaagtaatg gcaaagtgtc aacatgaaaa
cttagtagaa ctacttggtt tctcaagtga tggagatgac ctctgcttag tatatgttta
catgcctaata ggttcattgc tagacagact ctcttgcttg gatggtactc caccactttc
ttggcacatg agatgcaaga ttgctcaggg tgcagctaata ggcatacaatt ttctacatga
aaatcatcat attcatagag atattaaaaag tgcaaatatc ttactggatg aagcttttac
tgctaaaata tctgactttg gccttgcacg ggcttctgag aagtttgccc agacagtcac
gactagcaga attgtgggaa caacagctta tatggcacca gaagctttgc gtggagaaat
aacacccaaa tctgatattt acagcttttg tgtgggttta ctagaaataa taactggact
tccagctgtg gatgaacacc gtgaacctca gttattgcta gatattaaag aagaaattga
agatgaagaa aagacaattg aagattatat tgataaaaag atgaatgatg ctgattccac
ttcagttgaa gctatgtact ctgttgctag tcaatgtctg catgaaaaga aaaataagag
accagacatt aagaaggttc aacagctgct gcaagagatg acagcttctt aa

FIGURE 10A

MNKPITPSTYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSG
DDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCTVGDLDLLIQNEFFAPASLLLP
DAVPKTANTLPSKEAITVQQKQMPFCDKORTLMTPVQNLEQSYMPDSSSPENKSLEV
SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEFGGVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFS SDGDLCLVYVYMPNGSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLEIITGLPAVDEHRE
PQLLLDIKEEIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
QQLQEMTAS

FIGURE 10B

Death domains:

C. pneumoniae

DLWRQFALSLGVSEEEELANHEFSQAAQDMVATFRRLCDMPQLAVGLGALYTYEIQIPQVCVEKIR

C. muridarum

DLWKQFVFALGVSSSELEAHEPSEAAKAKVATFMRWCTGDSLAAGVAALYSYESQIPCVAKEKIR

C. psittaci

DLWKNFAYALGVTEEELENHVPSAAAQKKVDTFLRWCTGDSLSAGVAALYTYESQIPTVAETKIS

FIGURE 11A

GI:7190927

ORGANISM Chlamydia muridarum

ORIGIN

1 mesrkgikev smnflldqlda iiqnkhmleh pfymkwske ltkeqlqaya
kdyylhikaf
61 pkylsaihsr cddlearkll ldnlmdeeng ypnhidlwq fvfglgsse
eleahpsea
121 akakvatfmr wctgdslaag vaalysyesq ipcwakekir glieyfgfsn
pedyayfteh
181 eeadvrhare ekaliemlsr ddsdkvleas revtqslygf ldsflepatc
chchka

GI:7468151

ORGANISM Chlamydophila pneumoniae [Chlamydia pneumoniae]

ORIGIN

1 mtswiellldk qiedqhmlkh efyqrwsegk lekqqlqaya kdyylhikaf
pcylsalhar
61 cddlqirrqi lenlmdeeag npnhidlwrq falslgvsee elanhefsqa
aqdmvatfrr
121 lcdmpqlavg lgalytyeiq ipqvcvekir glkeyfgvsa rgyayftvhq
eadikhasee
181 kemlqtlvgr enpdavlggs qevldtlwnf lssfinstep csck

FIGURE 11B

6405 ttaagc tttgtgacaa
6421 tgacaacatg ttgcaggctc taaaaatgaa tccaaaaagc cgtataaaga ttgtgtaact
6481 tctcgcgaag ctctctaaaac tttgtcgccta tcatctcttag acaacatctc aattaaggcc
6541 ttttcttccc tagcatgacg cacatcagct tcttcatgct ccgtgaaata agcataatct
6601 tcaggattag aaaagccaaa gtactcaatc aatccacgaa ttttttcttt agctacgcaa
6661 ggaatttgac tttcataaga atacaaagcc gctactcctg ctgctaaaga atccccctgtg
6721 caccaccgca taaatgtcgc aaccttagct ttagctgctt cactgggttc atgagcttct
6781 agctcttctg aagacactcc aagagcaaac acaaattggt tccataaatc aatatgatta
6841 ggataaccat tctcttcatc cattaagtta tctaataata acttgcgggc ttctaaatca
6901 tcacaacggc tatgaatagc agataaatat tttggaaaag ctttgatatg caaatagtaa
6961 tcttttgcgt atgcctgtaa ttgttctttt gtcagctctc cttttgacca cttcatgtaa
7021 aaaggggtgt ctaacatag tttgttttga ataattgcat ctagctgac taaaaaatc
7081 atgctcacct cttttattcc ttttcttgat tccac 7115

FIGURE 11C

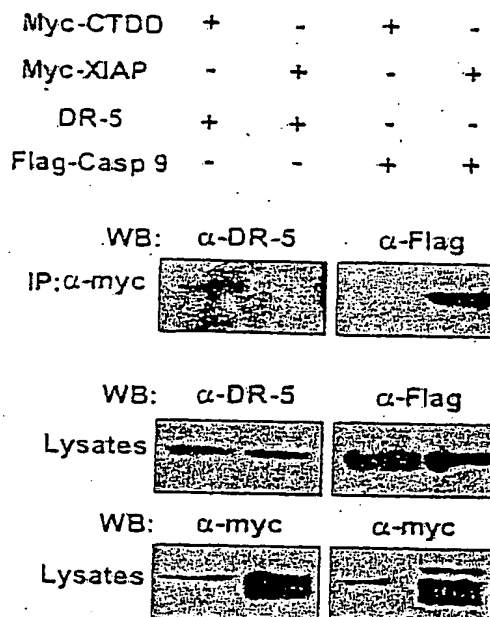


FIGURE 12

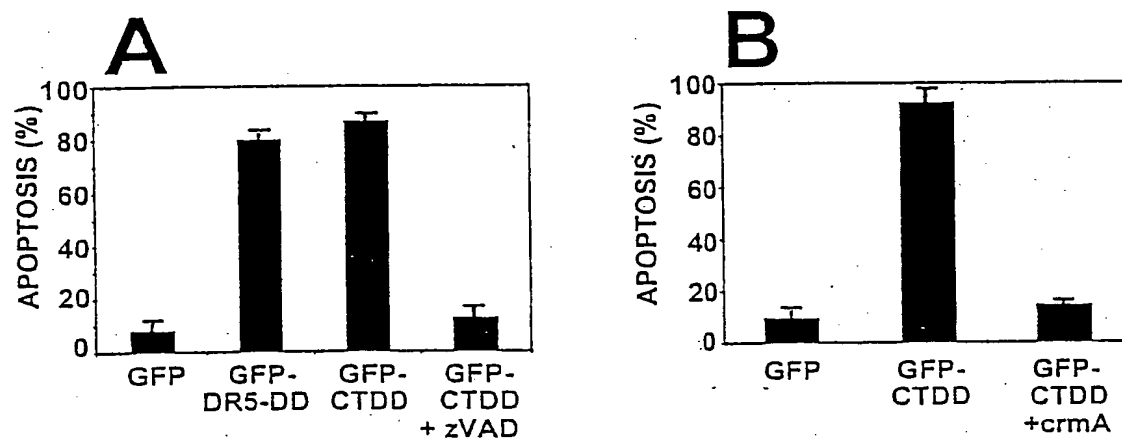


FIGURE 13

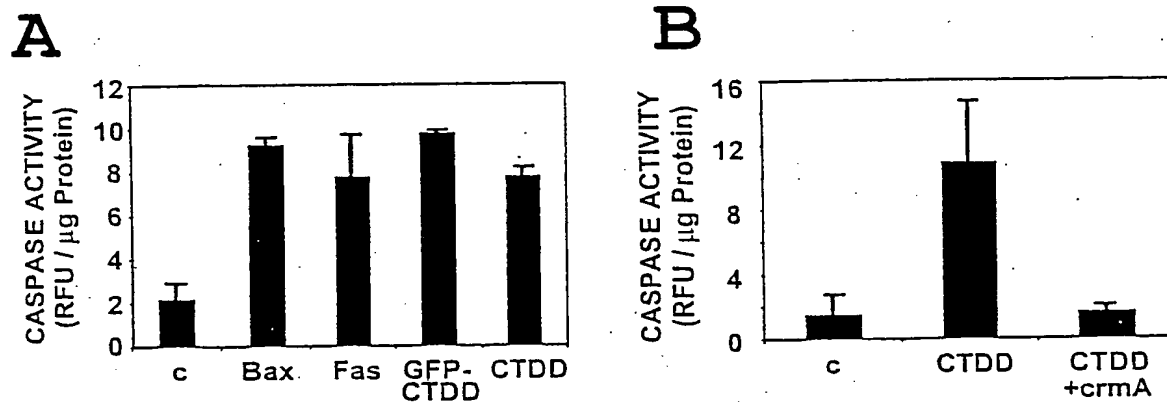


FIGURE 14

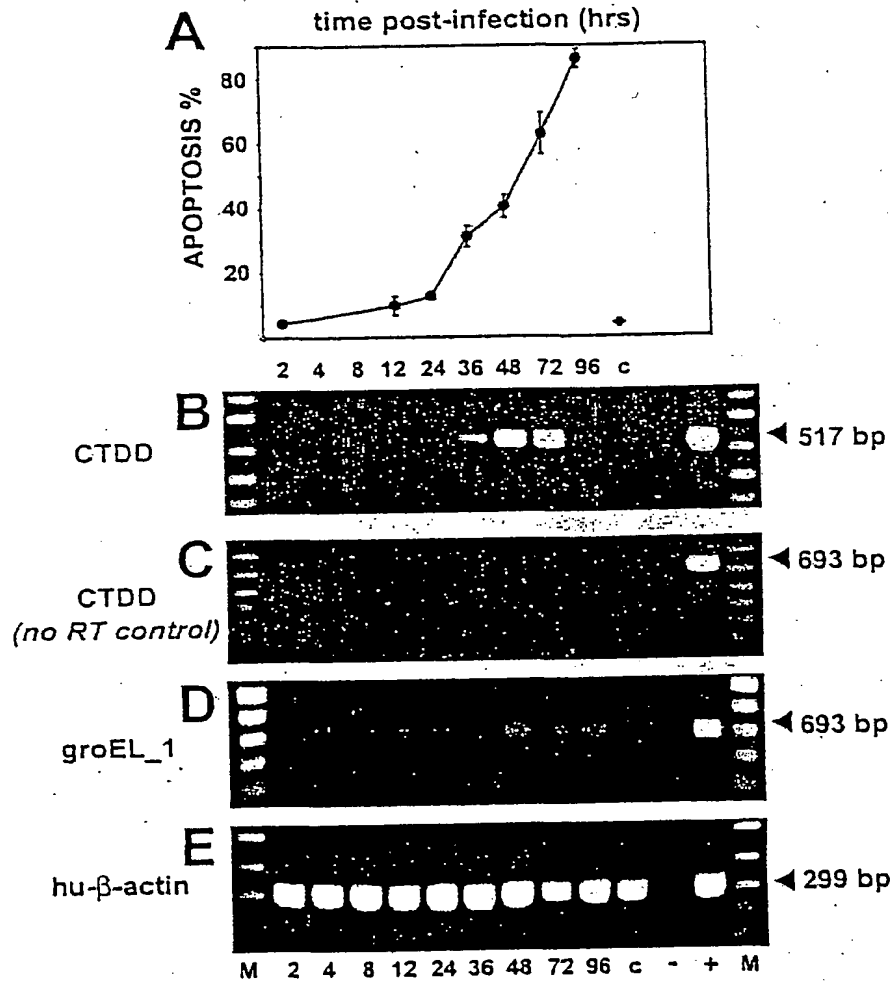


FIGURE 15